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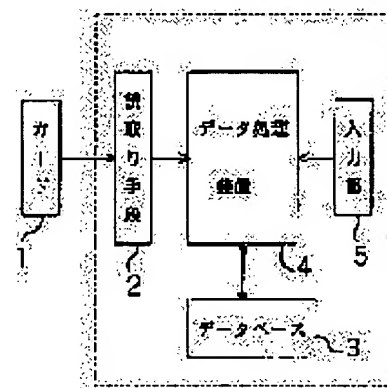
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(54) PERSON DISCRIMINATING SYSTEM BY DNA

(57)Abstract:

PROBLEM TO BE SOLVED: To reliably discriminate the fact of the person himself, and reliably prevent an unfair practice by comparing data of base sequence in DNA recorded on a recording body such as a card carried by a discriminating object person with preregistered data of base sequence in DNA of the person himself.

SOLUTION: First of all, a user inputs individual discriminating data such as a name and a code number from an input part 5 such as a keyboard, and compares and checks up this individual discriminating data with individual discriminating data preregistered on a database 3, and judges whether or not the user is the registered person himself. When both data coincide with each other, the user inserts a carried card 1, on which base sequence or the like in DNA is recorded, into a device, and reads data recorded on this card 1 by a reading means 2. It is compared and checked up with data on base sequence or the like in DNA of the person himself prestored in the database 3 by a data processor 4, and when they coincide with each other, various procedures such as repayment of a deposit or the like are permitted.



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DETAILED DESCRIPTION

[Detailed Description of the Invention]

[0001]

[Field of the Invention] This invention relates to the person discernment system by DNA, and the object is to offer a person discernment system without a possibility that it may be imitated and may be abused for others while being able to identify certainly that he is a principal.

[0002]

[Description of the Prior Art] In recent years, card society is realized and card society continues to be expected to grow up increasingly. However, the large-sized crime in connection with a card has also been increasing increasingly with growth of card society. As one of the big causes which cause such a card criminal fraud, it is mentioned that a problem is in the individual discernment approach. As a certain person identifying method, although there were the viewing method, a seal method, the signing method, cryptography, a fingerprinting method, etc., the trouble existed in the person identifying method of these existing for many years, respectively.

[0003]

[Problem(s) to be Solved by the Invention] As a trouble of the existing person identifying method which was described above By the seal method, others can also create the same seal and cannot check [that no persons other than an acquaintance can distinguish by the viewing method probably,] certainly whether you are a principal, In that others are able for there to be no means to recognize a sign promptly by the signing method, and to imitate, and cryptography, if a code leaks, it will be mentioned that there may be those who use the same code as semantics being lost. Moreover, since a fingerprinting method can identify an individual certainly, it is convenient apparently, but since the finger has always appeared in the table, possible, there is a bad image of a criminal investigation in a fingerprint, and it cannot say extracting and abusing a fingerprint as the best approach easily, either. Thus, the identification approach which the identification approach used conventionally is holding the trouble, respectively, and can be called best did not exist. Since the base sequence in the gene of DNA changed with individuals as a result of inquiring wholeheartedly about a person discernment system without a possibility that it may be imitated and may be abused for others while it was possible to have identified certainly that he is a principal in view of such the actual condition, this invention person came to create the person discernment system which used the means which carries out detection analysis of the record object of the base sequence of this gene, and it.

[0004]

[Means for Solving the Problem] This invention was used as the person discernment system by DNA characterized by identifying whether an identified person is a principal by comparing the data of the base sequence in DNA recorded on record objects, such as a card which the identified person brought, with the data of the base sequence in a principal's DNA beforehand registered into the database by invention which relates to claim 1 as above-mentioned The means for solving a technical problem. Moreover, in invention

concerning claim 2, it considered as the person discernment system by DNA characterized by identifying whether an identified person is a principal by comparing the data of the base sequence in the exon part of DNA recorded on record objects, such as a card which the identified person brought, with the data of the base sequence in the exon part of a principal's DNA beforehand registered into the database. In invention concerning claim 3, it considered as the person discernment system by DNA characterized by identifying whether an identified person is a principal by comparing the data of the base sequence in the intron part of DNA recorded on record objects, such as a card which the identified person brought, with the data of the base sequence in the intron part of a principal's DNA beforehand registered into the database. It considered as the person discernment system by the DNA characterized by to identify whether an identified person is a principal by comparing the data of the pattern obtained when electrophoresis of the DNA fragment recorded on record objects, such as a card which the identified person brought, in invention concerning claim 4 carries out with the data of the pattern obtained when electrophoresis of a principal's DNA fragment beforehand registered into the database is carried out.

[0005]

[Embodiment of the Invention] It explains referring to a drawing hereafter about the suitable operation gestalt of the person discernment system by DNA concerning this invention. Drawing 1 is the outline block diagram showing an example of the person discernment system by DNA concerning this invention. The record object with which the system of the example of a graphic display consists of a card (1) which recorded the base sequence in DNA which an identified person brings etc., A reading means to read the data recorded on the card (1) (2), The database with which data, such as a base sequence in a principal's DNA, are recorded beforehand (3), It consists of the input sections (5) for inputting the data processor (4) equipped with CPU which performs comparison collating with the data read in the card (1) while reading the data memorized by the database (3), and identification data, such as a name and a personal identification number.

[0006] Next, the person discernment system use approach by DNA concerning this invention is explained based on flow chart drawing shown in drawing 2. The person discernment system by DNA concerning this invention is applied suitable for equipments which need a user's identification, such as electronic keys, such as a bank, CD (cash dispenser) of a post office, ATM (automatic teller's machine) and the automatic agreement machine of a consumer finance company or a house, and a locker room, and the user of these equipments inputs identification data, such as a name and a personal identification number, first from the input section (5) which consists of a keyboard etc. Then, comparison collating of the inputted identification data, such as a name and a personal identification number, is carried out with the identification data beforehand registered into the database (3), and a judgment whether you are the principal by whom the user is registered is made. When input data is in agreement with registration data, a user inserts the card (1) which recorded the base sequence in brought DNA etc. in equipment. If a card (1) is inserted, the data recorded on the card (1) will be read by the reading means (2) of arbitration, such as a scanner, comparison collating will be carried out by the data and the data processors (4) in a principal's DNA beforehand memorized by the database (3), such as a base sequence, and a judgment whether you are the principal by whom the user was registered will be made. When a principal's data beforehand remembered to be data recorded on the inserted card (1) are in agreement, it is judged that he is a principal and it becomes possible to comply the cash drawer of a credit etc. with several formalities.

[0007] As record objects, such as a card (1) in this invention, a magnetic card, an IC card, etc. can use the record object of arbitration suitably. In addition, although mentioned later, when using the electrophoretic pattern of a DNA fragment itself as discernment data, it is good for a mere plastic card etc. also as whether the photograph of the pattern of electrophoresis is printed at the card face or the rear face, and a stuck thing. Moreover, what is necessary is just to use pattern reading means, such as a scanner, about a reading means (2), in using a magnetic card that what is necessary is just to set up according to the class of record object, using an IC card for the reading means of magnetic information and using the electrophoretic pattern of a

DNA fragment itself for the reading means of electronic intelligence as discernment data.

[0008] Either of the patterns obtained when electrophoresis of the base sequence in DNA, the base sequence in the exon part of DNA, the base sequence in the intron part of DNA, and the DNA fragment is carried out as data memorized by the record object and databases (3) in this invention, such as a card (1), is adopted. In addition, the part which it is joined together after the part of the structural gene as for which the manifestation of the genetic information of mammalian is cut off within a nucleus when messenger RNA is built from this messenger RNA precursor, although it starts when the genetic information of DNA is copied by the messenger RNA precursor, and an exon and the intron do not serve as a code is the intron and is shaved off, and builds messenger RNA is an exon.

[0009] DNA used as data is extracted from blood, a cell, hair, body fluid, etc. Although especially the extract approach is not limited but each approach better known than before can be used suitably, the extract approach as shown below as an example can be illustrated.

[0010] First, the dissolution of a cell and solubilization of DNA are performed as a first stage story. Ionicity or a nonionic surfactant is used for the dissolution of a cell. In addition, since the dissolution of a cell will promote decomposition of the extract DNA by nuclease etc., it is necessary to perform activity control of nuclease to a cell solution simultaneously using chelating agents, such as a disodium ethylenediaminetetraacetate monohydrate (EDTA). Next, since DNA exists in the form of DNA-protein complex, DNA is separated from protein using the proteinase K which is nonspecific protease.

[0011] Phenol processing is performed as a second stage story. Phenol processing is performed in order to denaturalize and to carry out separation clearance of the enzymes (proteinase K, RNase, etc.) added in the sample in the protein and the purification process of the sample origin. The nuclease of extent which it is here, and other protein denaturalize, and appear as precipitate in the interlayer of a phenol layer and a water layer. By this processing, DNA is extracted in the upper layer, i.e., a water layer, and separation from a protein component is finished. In addition, the mixture of chloroform, phenol chloroform, chloroform, and other organic solvents can also be used besides a phenol.

[0012] Alcoholic precipitate is performed as the third step. Alcoholic precipitate is performed for the object of clearance of mixture, such as concentration and the phenol of DNA in a solution, a salt, and a nucleotide, and it is carried out under mixture of the univalent cation of 0.1-0.5M. As alcohol, the ethanol of 2 double volume or the isopropanol (2-propanol) of the 0.6 time volume is used. DNA is recovered by this actuation as white precipitate.

[0013] Although DNA extracted by approach which was described above is used as data for identification, in the discernment system concerning this invention, the base sequence in the pattern and DNA which are obtained when electrophoresis of the DNA fragment is carried out, as mentioned above, the base sequence in the exon part of DNA, or the base sequence in the intron part of DNA is adopted as data for identification.

[0014] First, the case where the pattern obtained when electrophoresis of the DNA fragment is carried out is used as data for identification is explained. Electrophoresis is a phenomenon which will move toward cathode or an anode plate based on the difference of electrification which those matter has with the migration difference of a proper if suitable pH, the buffer solution, and a base material are chosen for the matter which has electrifications, such as protein and amino acid, and electric field are applied, and in this invention, a restriction enzyme cuts DNA, it fragments, and electrophoresis of the fragment is carried out in base materials, such as polyacrylamide gel. Then, the DNA fragment with negative charge moves toward an anode plate in the inside of gel. In order that a larger molecule may be caught in the hole of gel and may move late at this time, chain length's long fragment and chain length's short fragment are classified, and the pattern of a band is formed.

[0015] the specific nucleotide sequence of the palindrome of DNA intramolecular in many restriction enzymes -- recognizing -- the inside of the array -- or -- and a DNA strand is cut by number nucleotide detached building *****. Since the base sequence of DNA is peculiar to an individual, the part cut in case a restriction

enzyme cuts DNA will change with individuals, and the die length of the DNA fragment obtained becomes what changed with individuals. Therefore, the pattern of the band obtained by electrophoresis also becomes what changed with individuals, and the person discernment of it is attained by the comparison of this pattern. supposing drawing 3 is the mimetic diagram of the pattern obtained when electrophoresis of the DNA fragment is carried out, for example, (a) is a principal's pattern -- a principal -- the pattern of the person of an except becomes what is different as shown in (b) thru/or (c).

[0016] The following two technique can be illustrated as the technique of data-izing this pattern. The approach of evaluating the pattern of the obtained electrophoresis as the first technique, and using as data is mentioned. The approach of evaluating the ratio of the distance from the ratio of the distance between each band or distance or a start point to [from an electrophoretic pattern] each band or distance etc., and specifically using as data can be mentioned as an example. If the example of the electrophoretic pattern which showed this to drawing 4 explains briefly, as a distance between each band, numeric values, such as A:B, B:C, and C:D, will be used as discernment data as a ratio of distance, such as A, B, and C, as a ratio of a, b, c, d, e, and distance as a distance from start points, such as a:b, b:c, and c:d, to each band. The specific location where a band tends to appear in an electrophoretic pattern as an example of other approaches beforehand is set up, and when a band appears in this location, 1 and the approach which creates data as 0 in not appearing can also be used suitably. XA beforehand set up in drawing 4 when the example of drawing 4 explained concretely, XB, XC, XD, and XE (XC, 1) (XD, 1) Since the band has appeared altogether in the location, it is (XA, 1) (XB, 1) (XE, 1), It becomes data to say. And while making the discernment data obtained by approach which was described above register into a database, discernment of whether an identified person is a principal as shown in flow chart drawing of drawing 2 will be performed by making it record on record objects, such as a card, and passing the principal.

[0017] The second technique is the approach of using the pattern of the obtained electrophoresis itself as data. In this case, an identified person can identify whether you are a principal by sticking whether the photograph of the pattern of electrophoresis is printed at the card face or the rear face, passing the principal, reading a pattern using a scanner in the case of an activity, and comparing the data of the read pattern with the data of the pattern a principal's electrophoresis beforehand registered into the database.

[0018] Moreover, what is necessary is to analyze the base sequence of DNA beforehand extracted from the principal, to make it record on record objects, such as a card, and just to pass the principal, while making it register with a database by making this into person discernment data when using the base sequence in DNA as data for person discernment.

[0019] Specifically, the array of the base (nucleotide) in the intron part in DNA and the exon part which is a gene is registered into sequence from the 1st chromosome about 23 sorts of chromosomes at the database. On the occasion of registration, the part which shows the polymorphism in the genome which is the whole DNA which is in 23 chromosomes beforehand as for close, i.e., the remarkable part of individual difference, (polymorphism marker) is discovered. Thereby, in case the base sequence data of an identified person are compared with a principal's base sequence data, it can identify with a promptly and sufficient precision by specifying and comparing only the part where no base sequences are compared but ** also shows polymorphism. In this case, of course, it is desirable to discover the polymorphism marker which can discriminate an individual from few possible base sequences. Moreover, discernment precision can be raised by increasing the number of the polymorphism markers used in the case of a comparison.

[0020] Drawing 5 is the explanatory view showing an example of the suitable operation gestalt of the base sequence data registered into the database. The classification division of the base sequence data in the example of a graphic display is systematically carried out like [while consisting of Oita it is incomparable from the number of a chromosome, and a class of gene in a chromosome] the pole classification which shows the base sequence in a classification, the minor key which shows the exon section or the intron section of a gene, the exon section, or the intron section. And in case the base sequence data of an identified person are

compared with a principal's base sequence data, the individual difference known beforehand specifies a large polymorphism part, and should compare ejection and a base sequence only for the data of the part. If drawing 5 explains concretely, when it turns out that a polymorphism part with large individual difference is a part of * mark, for example, by comparing by specifying 1-P-E in the case of a data comparison, and reading only the data of * mark part, it is a short time and a person can be identified with a sufficient precision. At this time, two or more polymorphism parts may be specified and discernment precision can be raised by increasing a part for a specification part.

[0021] The approach of setting (01) and G (guanine) to (10), setting C (cytosine) to (11), transposing (00) and T (thymine) to a numeric value, and data-izing A (adenine) as the data-ized technique of a base sequence, for example can be illustrated. if the example of drawing 5 explains concretely -- the base sequence data of * mark part -- (... 01, 01, 00, and ...) -- it becomes.

[0022] In addition, although all base sequence data may be recorded on a database, it is good also as a configuration whose individual difference known beforehand takes up and records some data of only a large polymorphism part. Moreover, the same is said of record objects, such as a card.

[0023] in addition -- if genome analysis will progress in the future -- a group -- it also becomes possible to compare the large DNA field containing the change in the order of a list of a gene, or the number of copies, and DNA other than a gene etc., and to use it for person discernment.

[0024] In addition, the analysis approach of the base sequence of DNA is not limited at all, but each well-known approach currently used from the former, such as the MAKUSAMU gill box bird method, the plus subtracting method, and the chain stopping method, is adopted suitably.

[0025] Four bases, adenine (A) which are assembling DNA with the MAKUSAMU gill box bird method, Specific cutting to a guanine (G), a thymine (T), and a cytosine (C) A lifting, After being the approach of deciding the sequence of the base sequence of a DNA strand and carrying out the indicator only of one end of a DNA strand by radioactive **** (32P) by it, DNA is cut by the approach specific to each base at one rate to hundreds bases, the die length of a DNA strand separates using the after polyacrylamide gel electrophoresis, and a base sequence is read in distribution of 32P. After using a phosphatase enzyme on the phosphoric acid radical (5'-phosphoric acid) of the five prime end of a chain and removing this as an approach of carrying out the indicator of the end of a DNA strand, there is the approach of carrying out the indicator of the nucleotide of a 3'-end using the approach of setting a five prime end to 32P using the adenosine triphosphate (ATP) which carried out the indicator to the polynucleotide kinase by 32P, and the deoxyribonucleotide 3 phosphoric acid which carried out the indicator to DNA polymerase by 32P.

[0026] Moreover, by the plus subtracting method, the single strand of DNA which carries out involution of the DNA of 2 chains which are going to determine a base sequence first to ejection and its fragment which started the part with the restriction enzyme very much, and was obtained is separated, and four kinds of deoxyribonucleoside 3 phosphoric acid is added to this. Radioactive **** (32P) is combined with one of kinds [them] at this time. DNA of **** of phage T four is used as mold, and a DNA strand is expanded by making into a primer the DNA fragment cut down with the restriction enzyme. Next, if three kinds of deoxyribonucleoside 3 phosphoric acid (for example, deoxyadenosine 3 phosphoric acid is lacked) is added, expanding will stop at the place before [of the base (in this case, adenine) which the DNA strand did not add] one. This is minus. the base (in this case, adenine) which the DNA strand added, respectively when only one of four kinds of deoxyribonucleoside 3 phosphoric acid (in this case, deoxyadenosine 3 phosphoric acid) was added next -- by the way, expanding stops. This is plus. Dissociate in order of the die length of a DNA strand, applying each to polyacrylamide gel electrophoresis, an X-ray film is made to expose a radiation, and the location of a band is decided. And a base sequence can be read in the result of a combination experiment of plus and minus.

[0027] Moreover, by the chain stopping method, dideoxy ribonucleoside 3 phosphoric acid is used as a substrate of a DNA polymerase reaction. Although this nucleotide is added to the three-dash terminal of a

DNA strand by DNA polymerase, since the hydroxyl group (3' - OH) of 3' is lacked, DNA polymerase cannot combine the following nucleotide, and chain expanding after it cannot be performed. For example, when deoxyadenosine 3 phosphoric acid (dATP), deoxyguanosine 3 phosphoric acid (dGTP), deoxycytidine 3 phosphoric acid (dCTP), a lot of dideoxy thymidine 3 phosphoric acid (ddTTP), and a small amount of deoxythymidine 3 phosphoric acid (dTTP) are added, the thing of various die length stopped in the place where chain expanding serves as a thymine is obtained. Since a product will build a band in order of the magnitude if the same reaction is performed also about the dideoxy ribonucleoside 3 phosphoric acid of other bases, those products are put in order and it applies to polyacrylamide gel electrophoresis, a base sequence can be decided by reading it in order.

[0028] Moreover, the approach of using STM (scanning tunneling microscope), AFM (atomic force microscope), etc. may be adopted as an approach of determining the base sequence of DNA. Since the configurations of a molecule differ, respectively, four sorts of bases of DNA, an adenine (A), a guanine (G), a thymine (T), and a cytosine (C) fix to a substrate the single stranded DNA which the single stranded DNA which consists only of one kind of base beforehand is observed [single stranded DNA], and he investigates [single stranded DNA] the configuration of each base, and wants to investigate a base sequence next, and investigate the configuration of this DNA using STM or AFM. Since the configuration of four kinds of bases is already known, the configuration of a single stranded DNA shows the location of each base, and the base sequence of this DNA is known.

[0029]

[Effect of the Invention] Since it is a person discernment system by DNA characterized by to identify whether an identified person is a principal when this invention compares data, such as a base sequence in DNA recorded on record objects, such as a card which the identified person brought, with data, such as a base sequence in a principal's DNA beforehand registered into the database, as explained above, the effectiveness which describes below does so. Namely, the base sequence in DNA which changes with individuals as person discernment data, In order to use either of the patterns obtained when electrophoresis of the base sequence in the exon part of DNA, the base sequence in the intron part of DNA, and the DNA fragment is carried out, The role of a kind of code data with these data peculiar to an individual is played, and while it is possible to identify certainly that he is a principal, it becomes the extremely excellent person discernment system without a possibility that it may be imitated and may be abused for others.

[Translation done.]